

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

| | | |
|----------------|---|---|
| Applicant | : | Dutron et al. |
| Appl. No. | : | 10/527,387 |
| Filed | : | October 17, 2005 |
| For | : | USE OF FAMILY 8 ENZYMES WITH XYLANOLYTIC ACTIVITY IN BAKING |
| Examiner | : | Badr, Hamid R. |
| Group Art Unit | : | 1794 |

DECLARATION UNDER 37 C.F.R. §1.132

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

I, Thierry Dauvrin, declare and state:

1. I am Senior Research Manager at Puratos, N.V., the assignee of the above-referenced patent application, and am an inventor on the above-referenced patent application.
2. I am an expert in the field of enzymatic enhancement of bakery products. I have been head of the Research & Development Department of the Business Unit "Enzymes" of the Puratos Group for more than 10 years.
3. I am an inventor of 6 patents, have authored about 10 peer reviewed scientific papers and have given oral presentations at about 6 scientific meetings.
4. I am familiar with the above-referenced application, pending claims and current Office Action. I understand that the claims were rejected as allegedly being obvious over Fuglsang et al. (WO 02/19828 "R1"), in view of Collins et al. (J. Biol. Chem. 277:35133-35139,

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2002 "R2"), Olesen et al. (US 6,110,508) and JP 2001-245665 (machine translation). I have reviewed the pending claims and these references.

5. This Declaration is being submitted to demonstrate that the xylanase from *Bacillus halodurans* disclosed by JP 2001-245665 is not a family 8 enzyme. I performed a BLAST analysis of the amino acid sequence of the *B. halodurans* xylanase described in JP 2001-245665. The results, which are shown in Exhibit A, demonstrate that this enzyme exhibits 100 % sequence identity to another xylanase from *B. halodurans* and to a xylanase from *Bacillus firmus*, and 86 % sequence identity to a xylanase from *Paenibacillus* sp. DG-22, which are all three family 11 xylanases. From this analysis, I conclude that the xylanase disclosed in JP 2001-245665 is a family 11 xylanase, and is not a family 8 xylanase.

6. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

By: Thierry DAUVIRIN

Date: 2009/08/12



7623662
081109

BLAST Basic Local Alignment Search Tool

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Bacillus halodurans xylanase JP2001 245 665

Results for: kJ3017 None(210aa) [View](#)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

kJ3017

Description

None

Molecule type

amino acid

Query Length

210

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program

BLASTP 2.2.21+ [Citation](#)

References

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Reference - [compositionally score matrix adjustment](#)

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwal, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", *FEBS J.* 272:5101-5109.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [Multiple alignment](#) [New](#)

Search Parameters

| | |
|-------------------------|----------|
| Program | blastp |
| Word size | 3 |
| Expect value | 10 |
| Hlhit size | 10 |
| Gapcosts | 11,1 |
| Matrix | BLOSUM62 |
| Threshold | 11 |
| Composition-based stats | 2 |
| Filter string | F |
| Genetic Code | 1 |
| Window Size | 40 |

Database

| | |
|---------------------|----------------------|
| Posted date | Aug 11, 2009 5:42 PM |
| Number of letters | 3,244,132,065 |
| Number of sequences | 9,489,734 |
| Entrez query | none |

Karlin-Altschul statistics

| Params | Unapped | Gapped |
|--------|----------|--------|
| Lambda | 0.316054 | 0.267 |
| K | 0.131596 | 0.041 |
| H | 0.434666 | 0.14 |

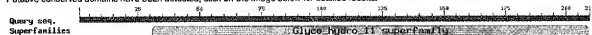
Results Statistics

| | |
|------------------------------|--------------|
| Length adjustment | 130 |
| Effective length of query | 80 |
| Effective length of database | 2010409182 |
| Effective search space | 160832732960 |
| Effective search space used | 160832732960 |

Graphic Summary

Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.

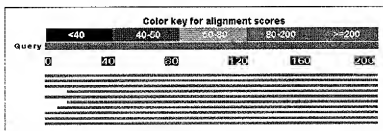


Distribution of 10 Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a

hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Description:

Sequences producing significant alignments:

| | Score | E |
|---|--------|-----------------|
| | (Bits) | Value |
| gcl:INP_241765.1 endo-1,4-beta-xylanhydrolase [Bacillus halodurans C-125] | 223 | 6e-117 G |
| gcl:BA04618.1 xylanase 11A [Bacillus firmus] | 222 | 1e-116 |
| gcl:IA012276.1 xylanase A [Paenibacillus sp. DG-22] | 223 | 2e-93 |
| gcl:IA04588.1 endo-beta-1,4-xylanase [Paenibacillus sp. ...] | 244 | 4e-93 |
| gcl:IA04588.1 endo-xylanase [Paenibacillus sp. H8] | 242 | 1e-92 |
| gcl:IA04588.1 RecName: Full=Endo-1,4-beta-xylanase A... | 163 | 2e-91 |
| gcl:IA04588.1 Endo-1,4-beta-xylanase [Geobacillus sp. 74] | 233 | 3e-90 |
| gcl:IA04588.1 beta-1,4-xylanase [Paenibacillus sp. M-61] d... | 227 | 5e-88 |
| gcl:IA04588.1 Endo-1,4-beta-xylanase [Paenibacillus sp....] | 222 | 6e-88 G |
| gcl:IA04588.1 xylanase I precursor [Acromonas punctata] | 236 | 8e-88 |

Alignments: Select All | Get selected sequences | Distance tree of results | Multiple alignments **new**

>ref|INP_241765.1| **G** endo-1,4-beta-xylanhydrolase [Bacillus halodurans C-125]
 dbj|BA04618.1| **G** endo-1,4-beta-xylanhydrolase [Bacillus halodurans C-125]
 gb|IA012276.1| endo-1,4-beta-xylanhydrolase [Bacillus halodurans]
 gb|IA04588.1| xylanase [Bacillus firmus]
 Length=210

Query ID: 493828 BH0899 | endo-1,4-beta-xylanhydrolase [Bacillus halodurans C-125] (Over 10 PubMed links)

Score = 423 bits (1087), Expect = 6e-117, Method: Compositional matrix adjust.
 Identities = 210/210 (100%), Positives = 210/210 (100%), Gaps = 0/210 (0%)

Query 1 MKFVFYKVLTVIAATISFCLSAVPASANTYQWYVTDGGGTVNAATNGPGNGVSVTRDGT 60
 Subject 1 MKFVFYKVLTVIAATISFCLSAVPASANTYQWYVTDGGGTVNAATNGPGNGVSVTRDGT 60
 Query 61 NFVVGKGEIWSGNRIHYNAAGVPSGNGVLYLYGTRNQLIEYVVDNNGVTRPTCTH 120
 Subject 61 NFVVGKGEIWSGNRIHYNAAGVPSGNGVLYLYGTRNQLIEYVVDNNGVTRPTCTH 120
 Query 121 RGTVSDGGTYDIYTHRYNAPSIDGOTFOQFWSVRQSKRPTGNVSVITFSHNVAWRN 180
 Subject 121 RGTVSDGGTYDIYTHRYNAPSIDGOTFOQFWSVRQSKRPTGNVSVITFSHNVAWRN 180
 Query 181 AGNGLGSSWSYQVLATGYQSSGRSNVTWV 210
 Subject 181 AGNGLGSSWSYQVLATGYQSSGRSNVTWV 210

>gb|IA083579.1| xylanase 11A [Bacillus firmus]
 Length=210

Score = 422 bits (1085), Expect = 1e-116, Method: Compositional matrix adjust.
 Identities = 209/210 (99%), Positives = 210/210 (100%), Gaps = 0/210 (0%)

Query 1 MKFVFYKVLTVIAATISFCLSAVPASANTYQWYVTDGGGTVNAATNGPGNGVSVTRDGT 60
 Subject 1 MKFVFYKVLTVIAATISFCLSAVPASANTYQWYVTDGGGTVNAATNGPGNGVSVTRDGT 60
 Query 61 NFVVGKGEIWSGNRIHYNAAGVPSGNGVLYLYGTRNQLIEYVVDNNGVTRPTCTH 120
 Subject 61 NFVVGKGEIWSGNRIHYNAAGVPSGNGVLYLYGTRNQLIEYVVDNNGVTRPTCTH 120
 Query 121 RGTVSDGGTYDIYTHRYNAPSIDGOTFOQFWSVRQSKRPTGNVSVITFSHNVAWRN 180
 Subject 121 RGTVSDGGTYDIYTHRYNAPSIDGOTFOQFWSVRQSKRPTGNVSVITFSHNVAWRN 180
 Query 181 AGNGLGSSWSYQVLATGYQSSGRSNVTWV 210
 Subject 181 AGNGLGSSWSYQVLATGYQSSGRSNVTWV 210

>gb|AB169991.1| xylanase A [Paenibacillus sp. DG-22]
 Length=211

Score = 345 bits (884), Expect = 2e-93, Method: Compositional matrix adjust.
 Identities = 173/211 (82%), Positives = 196/211 (93%), Gaps = 1/211 (0%)

Query 1 MKFVFYKVLTVIAATISFCLSAVPASANTYQWYVTDGGGTVNAATNGPGNGVSVTRDGT 59
 Subject 1 MKFVFYKVLTVIAATISFCLSAVPASANTYQWYVTDGGGTVNAATNGPGNGVSVTRDGT 59
 Query 60 GNFVVGKGEIWSGNRIHYNAAGVPSGNGVLYLYGTRNQLIEYVVDNNGVTRPTCTH 119
 Subject 60 GNFVVGKGEIWSGNRIHYNAAGVPSGNGVLYLYGTRNQLIEYVVDNNGVTRPTCTH 119
 Query 120 RGTVSDGGTYDIYTHRYNAPSIDGOTFOQFWSVRQSKRPTGNVSVITFSHNVAWRN 179
 Subject 120 RGTVSDGGTYDIYTHRYNAPSIDGOTFOQFWSVRQSKRPTGNVSVITFSHNVAWRN 179
 Query 180 AGNGLGSSWSYQVLATGYQSSGRSNVTWV 210
 Subject 180 AGNGLGSSWSYQVLATGYQSSGRSNVTWV 210

>ref|XP_04852431.1| endo-beta-1,4-xylanase [Paenibacillus sp. oral taxon 786 str. D14]
 gb|BS73597.1| endo-beta-1,4-xylanase [Paenibacillus sp. oral taxon 786 str. D14]
 Length=210

Score = 344 bits (882), Expect = 4e-93, Method: Compositional matrix adjust.
 Identities = 171/197 (86%), Positives = 184/197 (93%), Gaps = 1/197 (0%)

Query 15 ATISFCLSAVPASANTYQWYVTDGGGTVNAATNGPGNGVSVTRDGTGNFVVGKGEIWSG 73
 Subject 14 ASHSGFGLFATSAANDYQWYVTDGGGTVNAATNGPGNGVSVTRDGTGNFVVGKGEIWSG 73
 Query 74 NRTIYNAAGVPSGNGVLYLYGTRNQLIEYVVDNNGVTRPTCTHRTGTVSDGGTYDI 133
 Subject 74 NRTIYNAAGVPSGNGVLYLYGTRNQLIEYVVDNNGVTRPTCTHRTGTVSDGGTYDI 133
 Query 134 YTHRYNAPSIDGOTFOQFWSVRQSKRPTGNVSVITFSHNVAWRNAGNGLGSSWSYQV 193
 Subject 134 YTHRYNAPSIDGOTFOQFWSVRQSKRPTGNVSVITFSHNVAWRNAGNGLGSSWSYQV 193

sbjct 134 YTTMRYNAPSIDGTTGQQFWSVRQSRPTGNSVITFSNNHVNARKSKGMMLGSSSVQV 193

Query 194 LATGYQSSGRSNVTVM 210

sbjct 194 LATGYQSSGRSNVTVM 210

>gb|ABD66557.1| endo-xylanase [Paenibacillus sp. HY8]

Length=211

Score = 342 bits (877), Expect = 1e-92, Method: Compositional matrix adjust.
Identities = 171/211 (81%), Positives = 187/211 (88%), Gaps = 1/211 (0%)

Query 1 MFKFVKVLTVVIAATISFLSAVPAASANT-YWQVNTDGGGTVNATNGPGGNYSVTNRDT 59
MKFP K+LTVAA++SP + A +SA T YWQ NTDGGGTVNA NG GENVSVN++P

Sbjct 1 MFKFSKMLTLVLAASMSFGVFAATSSAATDYGQNTDGGGTVNATNGSGGNYSVTNRDT 60

Query 60 GNFVVGKGMELGSPNRTIYNAGVWNPSPSGNGYLLTGYTRNQLIEYVVDNGTGYRPTGT 119

SRFTVNRIT+YNAGVW NPSPSGNGYLLTGYTRNQLIEYVVDNGTGYRPTGT

Sbjct 61 GNFVVGKGMELGSPNRTIYNAGVWNPSPSGNGYLLTGYTRNQLIEYVVDNGTGYRPTGT 120

Query 120 HRCGTVSDGGTYDIYTTMRYNAPSIDGTTGQQFWSVRQSRPTGNSVITFSNNHVNARKSKGMMLGSSSVQV 179

+GTV SDGGTYDIYTTMRYNAPSIDGTTGQQFWSVRQSR PTG N +I FSNHVNARK

Sbjct 121 FAGTVNSUGGTGYDIYTTMRYNAPSIDGTTGQQFWSVRQSRPTGNSVITFSNNHVNARKSKGMMLGSSSVQV 180

Query 180 NAGNMLGSSWSYQVLATGYQSSGRSNVTVM 210

+ GKNLGSWSYQVLATGYQSSGRSNVTVM

Sbjct 181 SKGMMLGSSWSYQVLATGYQSSGRSNVTVM 211

>ep|P45705.2|XNLA_BACST RefName: Full=Endo-1,4-beta-xylanase A; Short=Xylanase A; AltName:

Full=1,4-beta-D-xylan xylanohydrolase A; Flags: Precursor

gb|AA071217.1| endo-beta-1,4-xylanase [Geobacillus thermoerophilus]

Length=210

Score = 338 bits (867), Expect = 2e-91, Method: Compositional matrix adjust.

Identities = 168/197 (85%), Positives = 182/197 (92%), Gaps = 1/197 (0%)

Query 15 ATISFLSAVPAASANT-YWQVNTDGGGTVNATNGPGGNYSVTNRDTGPNVVGKGLSP 73

ATISFLS L A T TGYNDGGGT VNA NGPGGNYSVTNRDTGPNVVGKGLSP

Sbjct 14 ASMSFLSGATSSAATDYGQNTDGGGTVNATNGPGGNYSVTNRDTGPNVVGKGLSP 73

Query 74 NRTIYNAGVWNPSPSGNGYLLTGYTRNQLIEYVVDNGTGYRPTGTGTHGTGYSD 133

NR I+YNAGVWNPSPSGNGYLLTGYTRNQLIEYVVDNGTGYRPTGTGTHGTGYSD

Sbjct 74 NRTIYNAGVWNPSPSGNGYLLTGYTRNQLIEYVVDNGTGYRPTGTGTHGTGYSD 133

Query 134 YTTMRYNAPSIDGTTGQQFWSVRQSRPTGNSVITFSNNHVNARKSKGMMLGSSSVQV 193

YTTMRYNAPSIDGTTGQQFWSVRQSRPTGNSVITFSNNHVNARKSKGMMLGSSSVQV

Sbjct 134 YTTMRYNAPSIDGTTGQQFWSVRQSRPTGNSVITFSNNHVNARKSKGMMLGSSSVQV 193

Query 194 LATGYQSSGRSNVTVM 210

sbjct 194 LATGYQSSGRSNVTVM 210

>ref|EP_03039720.1| Endo-1,4-beta-xylanase [Geobacillus sp. Y412MC10]

gb|EDV75913.1| Endo-1,4-beta-xylanase [Geobacillus sp. Y412MC10]

Length=203

Score = 333 bits (855), Expect = 5e-90, Method: Compositional matrix adjust.

Identities = 168/203 (82%), Positives = 182/203 (89%), Gaps = 1/203 (0%)

Query 9 LTVVIAATISFLSAVPAASANT-YWQVNTDGGGTVNATNGPGGNYSVTNRDTGPNVVGK 67

+TVVIAATISFLS A++SA T YWQ NTDGGGTVNA NG GENVSVN++P

Sbjct 1 LTVVIAATISFLSAVPAASANT-YWQVNTDGGGTVNATNGPGGNYSVTNRDTGPNVVGK 60

Query 68 WEIGSPNRTIYNAGVWNPSPSGNGYLLTGYTRNQLIEYVVDNGTGYRPTGTGTHGTGYSD 127

W GSPNRTI+YNAGVW NPSPSGNGYLLTGYTRNQLIEYVVDNGTGYRPTGTGTHGTGYSD

Sbjct 61 WNTGSPNRTIYNAGVWNPSPSGNGYLLTGYTRNQLIEYVVDNGTGYRPTGTGTHGTGYSD 120

Query 128 GGTGYDIYTTMRYNAPSIDGTTGQQFWSVRQSRPTGNSVITFSNNHVNARKSKGMMLGSSSVQV 187

GGTGYDIYTTMRYNAPSIDGTTGQQFWSVRQSR PTG N +I FSNHVNARKSKGMMLGSSSVQV

Sbjct 128 GGTGYDIYTTMRYNAPSIDGTTGQQFWSVRQSRPTGNSVITFSNNHVNARKSKGMMLGSSSVQV 180

Query 188 SWSYQVLATGYQSSGRSNVTVM 210

SWSYQVLATGYQSSGRSNVTVM

Sbjct 181 SWSYQVLATGYQSSGRSNVTVM 203

>dbj|BAE93061.1| beta-1,4-xylanase [Paenibacillus sp. W-61]

dbj|BAF49060.1| Xylanase I [Paenibacillus sp. W-61]

Length=211

Score = 327 bits (838), Expect = 5e-88, Method: Compositional matrix adjust.

Identities = 164/211 (77%), Positives = 184/211 (87%), Gaps = 1/211 (0%)

Query 1 MFKFVKVLTVVIAATISFLSAVPAASANT-YWQVNTDGGGTVNATNGPGGNYSVTNRDT 59

MKFP K+LTVAA++SP + A +SA T YWQ NTDGGGTVNA NG GENVSVN++P

Sbjct 1 MFKFSKMLTLVLAASMSFGVFAATSSAATDYGQNTDGGGTVNATNGSGGNYSVTNRDT 60

Query 60 GNFVVGKGMELGSPNRTIYNAGVWNPSPSGNGYLLTGYTRNQLIEYVVDNGTGYRPTGT 119

GPNVVGKGMELGSPNRTIYNAGVWNPSPSGNGYLLTGYTRNQLIEYVVDNGTGYRPTGT

Sbjct 61 GNFVVGKGMELGSPNRTIYNAGVWNPSPSGNGYLLTGYTRNQLIEYVVDNGTGYRPTGT 120

Query 120 HRCGTVSDGGTYDIYTTMRYNAPSIDGTTGQQFWSVRQSRPTGNSVITFSNNHVNARKSKGMMLGSSSVQV 179

+GTV SDGGTYDIYTTMRYNAPSIDGTTGQQFWSVRQSR PTG N +I FSNHVNARKSKGMMLGSSSVQV

Sbjct 121 FAGTVNSUGGTGYDIYTTMRYNAPSIDGTTGQQFWSVRQSRPTGNSVITFSNNHVNARKSKGMMLGSSSVQV 180

Query 180 NAGNMLGSSWSYQVLATGYQSSGRSNVTVM 210

+ GKNLGSWSYQVLATGYQSSGRSNVTVM

Sbjct 181 SKGMMLGSSWSYQVLATGYQSSGRSNVTVM 211

>ref|YP_030313364.1| Endo-1,4-beta-xylanase [Paenibacillus sp. JDR-2]

gb|ACV03278.1| Endo-1,4-beta-xylanase [Paenibacillus sp. JDR-2]

Length=211

Score = 327 bits (837), Expect = 6e-88, Method: Compositional matrix adjust.

Identities = 163/211 (77%), Positives = 180/211 (85%), Gaps = 1/211 (0%)

Query 1 MFKFVKVLTVVIAATISFLSAVPAASANT-YWQVNTDGGGTVNATNGPGGNYSVTNRDT 59

MKFP K+LTVAA++SP + L A +SA T YWQ NTDGGGTVNA NG GENVSVN++P

Sbjct 1 MFKLKKVMTVLAASMSFGVFAATSSAATDYGQNTDGGGTVNATNGSGGNYSVTNRDT 60

Query 60 GNFVVGKGMELGSPNRTIYNAGVWNPSPSGNGYLLTGYTRNQLIEYVVDNGTGYRPTGT 119

GPNVVGKGMELGSPNRTIYNAGVWNPSPSGNGYLLTGYTRNQLIEYVVDNGTGYRPTGT

```

Query 120 HRCITVSDGGTYDITVTMRVNAPSIDGTTQTFQPSVRSQSRPTCMNVNITFSNHNAMK 179
      ++GTV SDGGTYDITT R NAPSIDGT TF Q+WSVRQSRK TGRV+ITF+RHNAM+
Sbjct 121 YKCTVSSDGGTYDITTAQRVNAPSIDGTATFTQYWSVRQSRKATCSNVAITFANHNAMK 180

Query 180 NAGNMLGSSWSYQVLATEGYQSSGRSNVTVM 210
      + GSNLGSWSYQVLATEGYQSSG SRVTVM
Sbjct 181 SKGNMLGSSWSYQVLATEGYQSSGSRNVTVM 211

```

>dbj|BA006837.1| xylanase I precursor [Aeromonas punctata]
Length=211

Score = 326 bits (836), Expect = 8e-88, Method: Compositional matrix adjust.
Identities = 163/211 (77%), Positives = 166/211 (78%), Gaps = 1/211 (0%)

```

Query 1  MRFKFTVTLTVVIAATISFCLSAVPSANT-YKQVNTDGGGVNATNGPGQYGVTVWRT 59
      MRFKFT K+TVVIAA++SS +A +GA T YQV NTGGGVNA NG CONVSVA++T
Sbjct 1  MFKTKKKLMTVVLAAASMSFGVFAATSSAATDYQQRVTDGGGVNATNGSGQYGVSWQNT 60




Query 60  GNFVVGKQWELIGSPKRTIFBYNAGVWEPGNGYLTLYGWTRNQLIEYVVVDNMGITRPTGT 119
      GNFVVGKQW G+PWR ++YNAGV+ PSCNGYLT YGWTRN LIEYVVVD+NGITRPTGT
Sbjct 61  GNFVVGKQWGTGPRVNVNAGVFAISGNGYLTGYGWTNQLIEYVVVDNMGITRPTGT 120

Query 120 HRCITVSDGGTYDITVTMRVNAPSIDGTTQTFQPSVRSQSRPTCMNVNITFSNHNAMK 179
      ++GTV SDGGTYDITVTMRVNAPSIDGTTQTF Q+WSVRQSRKPTG N+ITFSNHNAM
Sbjct 121 YKCTVNSDGGTYDITVTMRVNAPSIDGTTQTFQYWSVRQSRKPTGVNSITFSNHNAMK 180

Query 180 NAGNMLGSSWSYQVLATEGYQSSGRSNVTVM 210
      + GM LG+SWSYQV+ATEGYQSSG +NVTVM
Sbjct 181 SKGNMLGSSWSYQVLATEGYQSSGRSNVTVM 211

```

Select All ☒ selected sequences ☐ Distance tree of results ☐ Multiple alignment ☒

NCBI  Protein  My NCBI  (Sign In) (Registered)

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Download ▼ Save ▼ Links ▼

NCBI Reference Sequence: NP_241765.1

endo-1,4-beta-xylanhydrolase [Bacillus halodurans C-125][Comment](#) [Features](#) [Sequence](#)

LOCUS NP_241765 210 aa Linear BCT 26-APR-2009

DEFINITION endo-1,4-beta-xylanhydrolase [Bacillus halodurans C-125].

ACCESSION NP_241765 GI:15613462

VERSION Project:235

DBLINK RefSeq: accession [NP_062579.2](#)

DBSOURCE

KEYWORDS

SOURCE

ORGANISM Bacillus halodurans C-125
Bacillus halodurans C-125
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

REFERENCE 1 (residues 1 to 210)

AUTHORS Takami,H., Nakasone,K., Takaki,Y., Maeno,G., Sasaki,R., Masui,N., Fuji,F., Hirama,C., Nakamura,Y., Ogawara,N., Kuhara,S. and Horikoshi,K.

TITLE Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and genomic sequence comparison with *Bacillus subtilis*

JOURNAL Nucleic Acids Res. 28 (21), 4317-4331 (2000)

FUNDED 11358122

REFERENCE 2 (residues 1 to 210)

AUTHORS Nakasone,K., Masui,N., Takaki,Y., Sasaki,R., Maeno,G., Sakiyama,T., Hirama,C., Fuji,F. and Takami,H.

TITLE Characterization and comparative study of the *rrn* operons of alkaliphilic *Bacillus halodurans* C-125

JOURNAL Extremophiles 4 (4), 209-214 (2000)

FUNDED 10870157

REFERENCE 3 (sites)

AUTHORS Takami,H. and Horikoshi,K.

TITLE Analysis of the genome of an alkaliphilic *Bacillus* strain from an industrial point of view

JOURNAL Extremophiles 4 (2), 99-108 (2000)

FUNDED 10605562

REFERENCE 4 (sites)

AUTHORS Takami,H., Takaki,Y., Nakasone,K., Sakiyama,T., Maeno,G., Sasaki,R., Hirama,C., Fuji,F. and Masui,N.

TITLE Genetic analysis of the chromosome of alkaliphilic *Bacillus halodurans* C-125

JOURNAL Extremophiles 3 (3), 227-233 (1999)

FUNDED 10421112

REFERENCE 5 (sites)

AUTHORS Takami,H., Masui,N., Nakasone,K. and Horikoshi,K.

TITLE Replication origin region of the chromosome of alkaliphilic *Bacillus halodurans* C-125

JOURNAL Biosci. Biotechnol. Biochem. 63 (6), 1134-1137 (1999)

FUNDED 10427224

REFERENCE 6 (sites)

AUTHORS Takami,H., Takaki,Y., Nakasone,K., Hirama,C., Inoue,A. and Horikoshi,K.

TITLE Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic *Bacillus* sp. strain C-125

JOURNAL Biosci. Biotechnol. Biochem. 63 (2), 452-455 (1999)

FUNDED 10192224

REFERENCE 7 (sites)

AUTHORS Takami,H., Nakasone,K., Ogawara,N., Hirama,C., Nakamura,Y., Masui,N., Fuji,F., Takaki,Y., Inoue,A. and Horikoshi,K.

TITLE Sequencing of three *lambda* clones from the genome of alkaliphilic *Bacillus* sp. strain C-125

JOURNAL Extremophiles 3 (1), 29-34 (1999)

FUNDED 10030642

REFERENCE 8 (sites)

AUTHORS Takami,H., Nakasone,K., Hirama,C., Takaki,Y., Masui,N., Fuji,F., Nakamura,Y. and Inoue,A.

TITLE An improved physical and genetic map of the genome of alkaliphilic *Bacillus* sp. C-125

JOURNAL Extremophiles 3 (2), 21-28 (1999)

FUNDED 10056841

REFERENCE 9 (sites)

AUTHORS Takami,H.

TITLE Genome analysis of facultatively alkaliphilic *Bacillus halodurans* C-125

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Sequence Analysis Tools

- BLAST Sequence
- Conserved Domains

Articles about the BH0899 gene

- Revision of the taxonomic position of the xylanolytic *B. (Extremophiles, 2002)*
- Cloning and characterization of two [Biochem Biophys Res Commun. 2004]
- Complete genome sequence of the alkaliphilic *B. (Nucleic Acids Res. 2000)*

See all...

Identical Proteins for NP_241765.1





- unnamed protein product [E [CAJ28966] halodurans]
- xylanase [Bacillus firmus] [AAQ14588]
- endo-1,4-beta-xylanhydrolase [AAO12276] halodurans]

See all...

More about the gene BH0899

Also Known As: BH0899

Protein Summary

-  xylanase Y [Bacillus halodurans]
-  bacillus halodurans xylan... (36)
-  endo-1,4-beta-xylanhydrolase [Bacillus halodurans C-125]
-  Protein Sequence (210)

See more...

Protein Summary

- BLINK
- Conserved Domains
- Full text in PMC
- Gene
- Genome Project
- Identical Proteins
- Nucleotide
- Protein Clusters
- PubMed (RefSeq)
- PubMed (Weighted)
- Related Structure
- Related Sequences

JOURNAL (in) Extremophiles in deep-sea environments (Ed.):
 : HORIKOSHI, K. TSUJII;
 : 249-264; Springer-Verlag (1999)

REFERENCE 10 (sites)
 AUTHORS Takami, H. and Horikoshi, K.
 TITLE Reidentification of facultatively alkaliphilic *Bacillus* sp. C-125
 to *Bacillus halodurans*

JOURNAL Biosci. Biotechnol. Biochem. 63, 943-945 (1999)

REFERENCE 11 (residues 1 to 210)
 CONSRSTM NCBI Genome Project
 TITLE Direct Submission
 JOURNAL Submitted (13-SEP-2001) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

REFERENCE 12 (residues 1 to 210)
 CONSRSTM NCBI Microbial Genomes Annotation Project
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2001) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

REFERENCE 13 (residues 1 to 210)
 AUTHORS Takami, H. and Takaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (22-MAR-2000) Japan Marine Science and Technology Center,
 Deep-sea Microorganisms Research Group, 2-15 Natsushima,
 Yokosuka,
 Kanagawa 237-0061, Japan

COMMENT PROVISIONAL [KSF250Q](#): This record has not yet been subject to
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 NCBI review. The reference sequence was derived from [BAB04918](#).

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
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GenBank: AAQ14588.1

xylanase [Bacillus firmus][Features](#) [Sequence](#)

LOCUS AAQ14588 210 aa linear BCT 01-NOV-2003
DEFINITION xylanase [Bacillus firmus].
ACCESSION AAQ14588
VERSION AAQ14588.1 GI:34451649
DBSOURCE accession [AF317713.1](#)
KEYWORDS .
SOURCE Bacillus firmus
ORGANISM *Bacillus firmus*
REFERENCE 1 (residues 1 to 210)
AUTHORS Chuensumzan, U., Ratanakhanokchai, K. and Cheevadhanarak, S.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-2000) Pilot Plant Development and Training Institute, King Mongkut's University of Technology Thonburi, Prachautit, Tungkr, Bangkok 10140, Thailand
COMMENT Method: conceptual translation.
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- BLAST Sequence
- Conserved Domains

Identical Proteins for AAQ14588.1

- unnamed protein product [E(CA129666) halodurans]
- endo-1,4-beta-xylanhydrolase [AAQ12276] halodurans]
- endo-1,4-beta-xylanhydrolase [NP_241765] halodurans C-125]

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- xylanase [Bacillus firmus]
- xylanase Y [Bacillus halodurans]
- [bacillus halodurans xylan...](#) (36)
- endo-1,4-beta-xylanhydrolase [Bacillus halodurans C-125]

[Protein Sequence \(210\)](#)
 let...

BLAST

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
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- Related Structure
- Related Sequences
- Domain Relatives
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GenBank: AB196991.1

xylanase A [Paenibacillus sp. DG-22][Features](#) [Sequence](#)

LOCUS AB196991 211 aa linear BCT 12-MAR-2007
DEFINITION xylanase A [Paenibacillus sp. DG-22].
ACCESSION AB196991
VERSION AB196991.1 GI:15394008
OBSSOURCE accession [J086596.1](#)
KEYWORDS .
SOURCE Paenibacillus sp. DG-22
ORGANISM *Paenibacillus sp. DG-22*
 Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
REFERENCE 1 (residues 1 to 211)
AUTHORS Lee, T.H., Lim, P.O. and Lee, Y.E.
TITLE Cloning, characterization, and expression of xylanase A gene from Paenibacillus sp. DG-22 in *Escherichia coli*
JOURNAL J. Microbiol. Biotechnol. 17 (1), 29-36 (2007)
PUBMED [18751380](#)
REFERENCE 2 (residues 1 to 211)
AUTHORS Lee, T.H., Lim, P.O. and Lee, Y.-E.
TITLE Direct Submission
JOURNAL Submitted (25-JUL-2006) Biotechnology, Dongguk University, Suksang-Dong 707, Kyongju, Kyongbuk 780-714, Korea
COMMENT Method: conceptual translation supplied by author.
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 //

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-  xylanase A [Paenibacillus sp. DG-22]
-  xylanase [Bacillus firmus]
-  xylanase Y [Bacillus halodurans]
-  [Bacillus halodurans xylan...](#) (36) Protein
-  [endo-1,4-beta-xylanhydrolase \[Bacillus halodurans C-125\]](#)

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